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HDLs in crises

Arnold von Eckardstein and Lucia Rohrer

Purpose of review

The clinical utility of HDLs has been scrutinized upon the publication of Mendelian randomization studies showing no effect of HDL-cholesterol (HDL-C) modifying variants on cardiovascular disease (CVD) outcome. The failures of randomized controlled HDL-C-directed intervention trials have further fueled this skepticism. This general criticism originates from oversimplification that has equated 'HDL-C' with 'HDL' and misconceived both as the 'good cholesterol'.

Recent findings

HDL particles are heterogeneous and carry hundreds of different lipids, proteins, and microRNAs. Many of them but not cholesterol, that is, HDL-C, contributes to the multiple protective functions of HDLs that probably evolved to manage potentially life-threatening crises. Inflammatory processes modify the composition of HDL particles as well as their individual protein and lipid components, and, as a consequence, also their functionality. Gain of dominant-negative functions makes dysfunctional HDL a part rather than a solution of the endangering situation. Quantification of HDL particle numbers, distinct proteins or lipids, and modifications thereof as well as bioassays of HDL functionality are currently explored toward their diagnostic performance in risk prediction and monitoring of treatment response.

Summary

Any successful clinical exploitation of HDLs will depend on the identification of the most relevant (dys)functions and their structural correlates. Stringent or prioritized structure-(dys)function relationships may provide biomarkers for better risk assessment and monitoring of treatment response. The most relevant agonists carried by either functional or dysfunctional HDLs as well as their cellular responders are interesting targets for drug development.

Keywords

cholesterol efflux, dysfunctional HDL, innate host defense, reverse cholesterol transport, sphingosine-1-phosphate bioassay

INTRODUCTION

Crises are 'specific, unexpected, and nonroutine events or series of events that [create] high levels of uncertainty and threat or perceived threat to an organization's high priority goals.' [1]. This definition is fulfilled by the role and fate of HDLs in both the life of an organism and medical research and development: HDLs help to prevent or manage crises of the organism caused, for example, by overload with cholesterol or xenobiotics, infectious or sterile inflammation, or injury [2]. For several decades, these properties as well as the association of low HDL-cholesterol (HDL-C) with increased cardiovascular risk [3,4] have generated considerable scientific interest in structure, function, metabolism, and regulation of HDL to exploit HDL for treatment and prevention of cardiovascular diseases (CVDs). Recent results of two lines of clinical or epidemiological research, however, led to a general critique of HDL's causal role in the pathogenesis

of atherosclerotic CVD and hence suitability as a therapeutic target. First, in randomized controlled trials, HDL-C increasing drugs – namely fenofibrate, nicotinic acid, and three inhibitors of cholesteryl ester transfer protein (CETP) – did not reduce cardiovascular event rates beyond statins [5]. Second, in Mendelian randomization studies, several polymorphisms or rare mutants were found associated with differences in HDL-C but not in cardiovascular risk [6]. These criticisms overlook the nonlinear relationship between HDL-C and cardiovascular risk

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KEY POINTS

- HDLs exert multiple functions that contribute to host defense from biological or chemical harm. These functions are exerted by HDL-holoparticles as well as specific agonists carried by HDL, for example, S1P. These properties make HDL interesting therapeutic targets even beyond prevention of CVDs.
- Inflammatory conditions modify both the composition and the structural components of HDLs. The resulting dysfunctional HDL particles not only lose protective functions but also gain noxious properties.
- Neither physiological function nor pathological dysfunction is recorded by the measurement of HDL-C. Novel biomarkers are currently searched and validated in clinical or epidemiological studies toward their potential to aid in drug development and improve risk prediction and monitoring of treatment response. Candidate biomarkers include HDL particle numbers, serum amyloid A, apoC-III, S1P, certain post-translational modifications of apoA-I, and cholesterol efflux capacity.
- The systematic elucidation of structure-function relationships of functional and dysfunctional HDL, for example, by a systems biology approach, may help to discover novel biomarker candidates as well as rationales and targets for therapeutic exploitation of HDL.

which according to meta-analyses is significant below the seventh decile only [3], the unsuitable design of most intervention studies which did not define HDL-C levels as inclusion/exclusion criteria, and the pleiotropic effects of the investigated drugs, which by also modulating plasma levels of LDL-cholesterol (LDL-C) and/or triglycerides do not allow any conclusion on the contribution of HDL-C to trial failure [7]. Most importantly, however, the cholesterol in HDL which is measured by HDL-C is neither the mediator nor the reporter of HDL function [2].

CRISIS PREVENTING AND SOLVING PROPERTIES OF HDLs

HDLs are heterogeneous and multimolecular complexes of hundreds of different molecules (proteins, lipids, microRNAs, and additional amphiphilic or lipophilic small molecules) [2]. Plasma concentrations of these molecules span four to five orders of magnitude and range from submicromolar [lipid transfer proteins, apoL1, sphingosine-1-phosphate (S1P)] to millimolar (cholesterol, phosphatidylcholine) [2]. Assuming HDL particle concentration of 20 $\mu\text{mol/l}$, an average HDL particle carries 50–100

molecules of cholesterol or phosphatidylcholine but less than 5% of the particles carry one molecule of the minor constituents. Already these numbers make clear that HDL-C cannot mirror the diversity and functionality of HDLs.

HDLs protect the function and survival of the organism by four different principle mechanisms.

Cholesterol efflux and reverse cholesterol transport

As the classical function, HDLs mediate transport of cholesterol from macrophage-foam cells to the liver for biliary excretion. HDLs elicit cholesterol efflux from cells via interaction with either ATP-binding cassette (ABC) transporters or scavenger receptor B1 (SR-B1) [2,8]. ABCA1-mediated phospholipid and cholesterol efflux was originally proposed to be elicited by prebeta1-HDL, that is, lipid-free apoA-I. The thereby generated discoidal nascent HDL particles as well as spherical mature HDLs produced by the subsequent esterification of cholesterol through lecithin:cholesterol acyltransferase (LCAT), were postulated to interact with SR-B1 and ABCG1 [2,8]. Recent systematic studies revealed that small dense HDL particles and lipid-free apoA-I are the most efficient mediators of cholesterol efflux [9], whereas ABCG1 did not contribute much to cholesterol efflux to small HDLs and little to cholesterol efflux to large HDLs. It rather appeared to mediate transport of cholesterol from intracellular pools to the plasma membrane [9].

Reverse cholesterol transport (RCT) is of special relevance for the removal of cholesterol from macrophages [2,8,10]. These cells of the innate immune system can bypass the down-regulated LDL receptor and take up modified lipoproteins through scavenger receptors, cells, and their debris as well as cholesterol crystals by different mechanisms of engulfment (phagocytosis, efferocytosis, pinocytosis) [10]. Cholesterol-loaded macrophage foam cells exert several proinflammatory activities. Thus, cholesterol loading of macrophages may have evolved to support host defense to combat acute infections and injuries [10]. However, if not resolved, this reaction propagates the pathogenesis of chronic inflammatory diseases, including atherosclerosis [10]. Cholesterol efflux by HDLs was shown to interfere with cytokine release. HDL-mediated cholesterol efflux may hence have evolved to resolve inflammation. In this regard, the opposite handling of cholesterol by LDL and HDL in inflammation is in analogy with the opposite action of different products of lipoxygenases and cyclooxygenases in inflammation, that is, lipoxins vs. leukotrienes and resolvins vs. prostaglandins, respectively [11].

Cholesterol efflux and RCT are probably also important means to compensate the dynamic and dramatic changes of cholesterol content in adipocytes elicited by the shrinkage of biomembranes surrounding lipid droplets during lipolysis [12]. In cells with less extreme alterations of cholesterol content, subtle HDL-induced changes in cellular cholesterol homeostasis have been associated with several changes of cellular differentiation and functions [10[•],13].

Signal transduction

HDLs elicit signal transduction processes which regulate the differentiation and egress, proliferation, survival, and function of various cell types [14]. In the context of host defense, the convergence of different HDL-induced cellular responses help to limit the inflammatory action of myelocytes and lymphocytes [11,15^{••}], provide integrity and functionality of endothelial barriers [16], secure energy homeostasis by stimulating insulin synthesis and secretion by pancreatic beta cells as well as glucose uptake by adipocytes and myocytes [17,18], stimulate angiogenesis [19], limit organ damage, and facilitate wound healing [20].

The cellular responses happen as the result of altered cholesterol homeostasis in specific plasma membrane domains, or specific agonist-receptor interactions activating signal transduction cascades. In this regard, HDL/SR-BI and apoA-I/ABCA1-interactions appear ambiguous. For example, the interaction of HDLs with SR-B1 activates kinases via its PDZ domain [14] or elicits cellular responses by altering the cholesterol content of specific plasma membrane domains that are enriched with signaling molecules such as endothelial nitric oxide synthase (eNOS) in caveolae of endothelial cells [13]. Likewise, the interaction of apoA-I with ABCA1 has been proposed to elicit cellular responses such as facilitated insulin secretion from beta cells or inhibited cytokine secretion from macrophages both indirectly by altering cellular cholesterol homeostasis via cholesterol efflux and directly by eliciting signal transduction, for example, through recruitment of heterotrimeric G-protein G α_s subunits or induction of signal transducer and activator of transcription 3 phosphorylation [14,17,18].

S1P is an example of less ambiguous agonist/receptor interactions: S1P is enriched in about 5% of plasma HDL particles by binding to apoM and interacts with five different G-protein coupled S1P receptors [14,21]. Apart from mediating the quantitative enrichment of S1P in HDLs, apoM does also act as a chaperone that modulates the quality of S1P/S1P receptor interactions. ApoM-bound and hence

HDL-carried S1P but not albumin-bound S1P was found to inhibit the differentiation, proliferation, and egress of murine lymphocytes as well as the suppression of NF- κ B and intercellular adhesion Molecule 1 (ICAM-1) in endothelial cells [10[•],17,22[•]]. In endothelial cells S1P promotes nitric oxide production, junction closure, cell proliferation and migration, as well as angiogenesis and inhibits apoptosis as well as TNF α -induced expression of vascular cell adhesion molecules [12,21]. S1P also promotes the survival of cardiomyocytes, hearts, and kidneys which are exposed to hypoxia, ischemia-reperfusion injury, or toxic drugs [14,21,23]. Some of these activities are also exerted by S1P-free reconstituted HDLs. However, the addition of S1P enhances the ability of S1P-free reconstituted HDL to protect hearts from ischemia reperfusion injury [23]. Moreover, HDLs were found to stimulate S1P efflux from erythrocytes in both apoM-dependent and apoM-independent manner. Initially, S1P-free or S1P-poor HDLs may hence be loaded with S1P during incubation with cells [24,25[•]]. As the alternative to this mediation of autocrine and paracrine effects, S1P-free and S1P-containing HDLs may elicit identical cellular responses by alternative mechanisms. Such mechanistic redundancy, however, is another indication for an important physiological role of HDLs.

Inactivation of extracellular biohazards

By its amphiphilic nature, HDLs can bind bacterial lipopolysaccharides, oxidized lipids as well as xenobiotics [26]. In this respect, it is interesting to note that HDLs have been isolated from several body fluids that separate cells from their external environment, for example, tears, nasal fluid, saliva, and bronchial fluid. [26] The intestine is even producing HDLs by itself [27]. Potentially hazardous molecules, including cholesterol are either eliminated by reverse transport to the liver or inactivated directly on the surface of HDLs [26]. The best investigated example for the latter situation is the hydrolysis of oxidized phospholipids, which are transferred by CETP or phospholipid transfer protein from LDLs to HDLs [28], by paraoxonase 1 (PON1), lipoprotein associated phospholipase A2, and lecithin:cholesterol acyltransferase. Notably, the antiatherogenic effect of PON1 is supported by data from clinical and epidemiological observational studies as well as genetic mouse models with knock-out or overexpression of PON1 [29].

Apart from inactivating or eliminating potentially noxious agents, the amphiphilic structure and specific molecules carried by HDLs also help to counteract downstream adverse effects of

inflammation, for example, complement activation, coagulation, and platelet aggregation. Some of these effects are exerted by apoA-I/phosphatidylcholine complexes, for example, the prevention of von Willebrand factor's self-association [30] or complement activation by cholesterol crystals [31]. Others are mediated by specific inactivators or inhibitors carried by HDLs, for example, the complement lysis inhibiting factor clusterin, antiproteolytic serpins, or the anticoagulant protein S [32,33].

Cellular uptake of HDLs or HDL components

HDLs deliver cargo to cells either by selective uptake, that is, independently of the entire particle, or via holoparticle uptake. Apart from mediating selective uptake of lipids from HDLs into liver and steroidogenic organs, SR-BI also facilitates the transfer of other HDL-associated molecules to cells, for example, microRNAs (miRNAs). In-vitro HDLs were found to deliver miRNAs to hamster baby kidney cells and human hepatocytes through SR-BI [34]. HDL-mediated delivery of miR-223 into endothelial cells was found to suppress ICAM-1 [35]. However, these findings are in contrast to those by Wagner *et al.* [36] who confirmed the presence of low copy numbers of miRNAs in HDLs, but found no evidence that HDLs deliver functionally relevant amounts of miRNAs into endothelial cells, smooth muscle cells, or monocytes [36]. Wagner *et al.* [36] found 10 000 copies of miR223 per μg HDL, that is, about 10 pmol HDL particles. The concentration of miR223 is hence 7 to 8 orders of magnitude below HDL particle concentration. The delivery of sufficient numbers of miRNA molecules for interference with several RNA molecules will require the interactions of a large number of HDL particles with a single cell. If at all this will more likely happen by autocrine or paracrine regulation of neighboring cells, that is locally, by using HDLs as a shuttle of secreted miRNAs as it has been described for exosomes [37], rather than by endocrine regulation of distant organs.

HDLs are also internalized by various cells, including hepatocytes, monocyte-derived macrophages, enterocytes, and endothelial cells [38]. ApoA-I has been shown to stimulate the uptake of HDL particles into hepatocytes and endothelial cells by activating the ectopic F1-ATPase/P2Y receptor axis [39]. In mice, the knock-out of P2Y13, which activates hepatic HDL uptake, impaired RCT from macrophage to feces and enhanced atherosclerosis despite counter-balanced SR-BI upregulation [40[¶]]. The potential clinical relevance of this F1-ATPase/P2Ys axis in humans is indicated by the

identification of serum F1-ATPase inhibitor (IF1) as an independent determinant of HDL-C and coronary heart disease (CHD) risk [41].

In mice, the cubilin/megalin complex mediates the uptake of HDL-like particles from the primary urine into tubular epithelial cells of the kidney. The knock-out of cubilin leads to decreased plasma levels of HDL-C in mice suggesting that this pathway may rescue some HDLs from renal degradation [42]. Interestingly, the knock-out of megalin or proteins regulating tubular endocytosis as well as the knock-out of apoM, which is a ligand of cubilin/megalin, led to the urinary excretion of S1P [24].

Our and other labs provided evidence that HDL-holoparticle uptake plays an important role for transport of HDLs through endothelial barriers, for example, into the vascular wall or into the brain [43,44]. Cultured endothelial and epithelial cells were observed to store HDLs or HDL components within intracellular vesicles [43,45[¶]] suggesting that HDLs or its components also fulfil intracellular functions. In fact, internalization of HDL is a prerequisite for the killing of *Trypanosoma brucei* by apoL1 [46]. Recently, internalization of HDLs with concomitant recruitment of phosphorylated I κ B kinase into autophagosomes was suggested as a means of preventing the TNF α -mediated activation of NF- κ B in the enterocyte cell line T84 and as a mechanism by which knock-out of apoA-I and transgenic overexpression of human apoA-I enhanced and suppressed, respectively, the intestinal inflammation in a mouse model of inflammatory bowel disease [45[¶]].

PERSISTING CRISIS LEADS TO HDL DYSFUNCTION

Very similar to the classical components of the immune system, the functionality of HDLs appears to be compromised by acute and chronic inflammatory conditions as well as metabolic decompensation, including infections, rheumatic and autoimmune diseases, CHD, diabetes, chronic kidney disease, or familial hypercholesterolemia [2,47]. The broad spectrum of HDL dysfunctions include reduced capacities to stimulate cholesterol efflux from macrophages, to inhibit LDL oxidation, apoptosis and, in endothelial cells, nitric oxide production, monocyte chemoattractant protein 1 as well as VCAM expression [2,16,47]. The structure-function relationships of HDL dysfunction (but also physiological function) are not comprehensively elaborated. Several dysfunctions have been associated with different molecules within HDLs. For example, endothelial HDL dysfunctions

have been assigned to the loss of S1P, plasmalogens, or clusterin, enrichment with serum amyloid A (SAA), apoC-III, or symmetric dimethylarginine, as well as oxidative modifications of apoA-I or phospholipids [2,16,25[■],47–50,51[■]]. Differences in cholesterol efflux capacity (CEC) have been attributed to alterations in HDL particle number, HDL subclass distribution, the kinetics of HDL/apoA-I exchange, in phospholipid composition, the accumulation of SAA, or post-translational modifications of apoA-I [2,47,52–59,60[■]]. As yet, villains and bystanders are not unequivocally discriminated.

In bioassays, most dysfunctions are recorded as reduction of normal functionality [2,47]. Beyond this apparent loss of function, HDLs of patients with CHD or chronic kidney disease were found to inhibit rather than stimulate nitric oxide production because they gained the ability to interact with the lectin-like oxidized LDL receptor LOX-1 and the Toll-like receptors TLR2 and TLR4, respectively, and thereby induced the phosphorylation of inhibitory rather than activating sites in eNOS [49,50]. Also SAA enrichment was found to generate noxious HDLs which in endothelial cells inhibit nitric oxide production and stimulate the production of reactive oxygen species as well as the expression of vascular cell adhesion molecule 1 [51[■]]. These findings raise the question whether also apparent loss-of-functions are caused by dominant negative effects. For example, the myeloperoxidase-mediated oxidation of Tyr-192 or Trp-72 residues in apoA-I which has been related to decreased CEC, affects about 20% of apoA-I in atherosclerotic plaques but only 0.02% of apoA-I molecules in plasma of CHD patients [56,57]. By loss of function, these modifications may limit macrophage cholesterol efflux locally within the arterial wall and contribute to the pathogenesis of atherosclerosis. However, the quantitatively very minor alterations can only markedly reduce CEC of total or apoB-free plasma, if they inhibit the cellular cholesterol efflux machinery. Interestingly, the injection of myeloperoxidase-oxidized apoA-I into mice decreased HDL-C levels and RCT from macrophages into plasma, whereas injection of nonoxidized apoA-I increased both HDL-C and RCT [58]. Likewise, the injection of HDLs of CKD patients increased blood pressure in mice [50]. The decreased CEC of HDLs enriched with SAA was explained by enhanced affinity to proteoglycans which prevents the access of HDLs to the plasma membrane [60[■]]. These examples are the first indications that gain of dysfunction converts originally protective HDLs into noxious particles.

CRITICAL FINDINGS IN EPIDEMIOLOGICAL AND CLINICAL RESEARCH

By contrast to previous studies [3,4], several recent studies did not find the inverse association between HDL-C and CHD events in patients with chronic or acute CHD [60[■],61,62]. Also a systematic comparison of associations between lipid risk factors and CHD events in three US-American population studies found the association of HDL-C (but also other lipid risk factors) with incident CHD weakened in the contemporary studies with baseline levels assessed between 2003 and 2007 as compared with the older atherosclerosis risk in communities (ARIC) study (with baseline levels assessed between 1988 and 1997) [63[■]]. The authors made the more prevalent statin use responsible for this secular trend. An alternative or additional explanation may be the changes in the methodology of HDL-C determination: the nowadays used homogenous assays for the determination of HDL-C (but also LDL-cholesterol) are notoriously inaccurate especially in dyslipidemic samples [64,65].

The negative results of randomized outcome trials on the add-on statin therapies with fenofibrate, niacin, or CETP inhibitors are frequently used arguments against the causal role and hence therapeutic suitability of HDLs [6]. However, in the randomized trials the effects of niacin or fenofibrate on HDL-C levels were rather modest (<10%). Moreover, with the exception of dalcetrapib [59], all drugs also beneficially affect LDL-C and lipoprotein(a) (niacin, torcetrapib, evacetrapib) and triglycerides (niacin and fenofibrate) [7]. These intervention trials hence do not allow any conclusion on the causal contribution of HDL-C to their failure. According to a recent meta-analysis, fibrates and niacin prevented cardiovascular events in the absence of statins but not if combined with statins [6]. Post hoc analyses revealed that patients with low HDL-C (<35 mg/dl/ <0.9 mmol/l) and hypertriglyceridemia (>200 mg/dl/ >2.3 mmol/l) benefit from treatment with fibrates independently of whether or not they were combined with statins [66]. Genetic post hoc analyses of the dal-OUTCOME study identified genetic differences in the adenylate cyclase 9 locus (ADCY9) as discriminators of dalcetrapib's efficacy [67[■]]. Dalcetrapib treatment decreased the cardiovascular event rate by 39% in patients with the AA genotype at rs1967309 of the ADCY9 locus but increased cardiovascular event rates by 27% in patients with the GG genotype [67[■]]. Randomized trials in such preselected patient groups are needed to prove that personalized treatment of patients with the low HDL-C/hypertriglyceridemia syndrome with fibrates or with the AA genotype at rs1967309 with a CETP inhibitor is effective.

Mendelian randomization studies provided evidence that associations with CHD risk of LDL-C, lipoprotein(a), and triglycerides but not with HDL-C are causal. Genetic mutants or polymorphisms that are associated with differences in HDL-C were not found associated with any differences in the prevalence or incidence of CHD events [5]. CETP polymorphisms are an exception in this regard. Carriers of CETP alleles associated with low CETP activity and, as the consequence, higher levels of HDL-C as well as lower levels of LDL-C and triglycerides have reduced risk of CVD [68,69]. It has been argued that these associations are driven by the effects of the polymorphisms on triglycerides and LDL-C [68]. However, it is important to recall that these polymorphisms like pharmacological CETP inhibitors primarily affect CETP activity and only secondarily lipid traits. The failures of torcetrapib, dalcetrapib [6,62], and possibly also evacetrapib [70] to reduce CHD event rates indicate that inborn and acquired decreases in CETP activity may have a different impact on CHD. This example points to limitations of the genetic strategy to predict outcome of pharmacological intervention.

Observational studies also found inverse associations between HDL-C and risks of ischemic stroke [3,71], progression of aortic aneurysm [72], incidence of diabetes mellitus [17,73,74], breast cancer [75] and colorectal cancer [76], as well as fatality of sepsis [77]. Although statistically independent of potential confounders, these associations also raise questions on causality. Two Mendelian randomization studies came to opposite conclusions on the causal association of low HDL-C with increased risk of diabetes mellitus: In the Copenhagen City Heart Study HDL-C levels but not genetic polymorphisms that influence HDL-C were found associated with incident diabetes mellitus [73]. By contrast, a meta-analysis of 140 single nucleotide polymorphisms known to affect plasma lipids found both measured and genetically determined elevations of HDL-C levels were found associated with decreased risk of diabetes mellitus [74]. Age-related macular degeneration provides an opposite example, where risk increases with increasing HDL-C [78]. The 442Gly encoding allele of the CETP gene which increases HDL-C and decreases CHD risk was found associated with elevated risk of age-related macular degeneration in an East Asian population [79].

STRATEGIES TO COPE WITH THE CRITICAL CLINICAL UTILITY OF HDLS

As HDL-C is no longer accepted as a surrogate marker for drug development, biomarkers that reflect HDL function are searched. Such biomarkers

must not only show diagnostic or prognostic superiority over HDL-C as well as modifiable risk association but they must also be technically feasible in terms of preanalytical requirements, accessibility, and turnaround time as well as analytically well controlled in terms of precision, accuracy, and traceability [80,81]. As yet most criteria are either not fulfilled or not proven by novel HDL biomarkers.

HDL particles and subclasses

Particle numbers and size subclasses of HDLs can be determined by NMR spectroscopy and ion mobility. Nondenaturing gradient gel electrophoresis and agarose gel electrophoresis differentiate HDL subclasses by size and charge, respectively. The subclasses as determined by the different technologies cannot be simply interconverted but a consensus was reached that distinguishes five HDL subclasses by size [82]. By contrast to HDL subclasses, HDL particle numbers (HDL-P) as determined by NMR showed rather consistent inverse associations with risk of CHD events [83]. However, only some studies showed superiority of HDL-P over HDL-C (multiple risk factor intervention trial, multi-ethnic study of atherosclerosis (MESA), Dallas Heart Study, the Rosuvastatin arm of JUPITER) [84–87], whereas others did not (Women's Health study, community-based cohort study (CMCS) Beijing project, EPIC Norfolk, and the placebo arm of JUPITER) [87–90]. Interestingly, the CMCS Beijing project found the HDL-C/HDL-P ratio positively associated with the progression of carotid atherosclerosis [89]. This observation was also made in MESA and may indicate dysfunction of cholesterol-overloaded HDL particles or impairment in RCT. This is also indicated by the association of cholesterol-enriched particles with increased risk of CHD and reduced CEC in patients with high HDL-C levels [55]. Although MESA proved superiority of HDL-P, the use of HDL-P together with LDL-P did not improve overall risk prediction by the American Heart Association/American College of Cardiology calculator score [91]. Also of note, in the JUPITER study, HDL-P as determined by NMR but not as determined by ion mobility was associated with incident CHD [92]. Finally, it is important to note that most published data from outcome studies were obtained by the NMR method developed by LipoScience which is now commercialized as LipoProfile. At least three alternative NMR-based methods for HDL-P determinations use different algorithms for the analysis of NMR signals [93–95]. Two of them are also commercialized (LipoScale and LipoFit) [93,94]. LipoProfile and LipoScale yield HDL-P concentrations that show mean deviations of more than

60% from each other as well as discrepant correlations with HDL-apoA-I levels [93]. Systematic method comparisons and large observational studies are needed for all methods to harmonize HDL-P determination and to prove the diagnostic value of HDL-P independently of the method used.

Bioassays of HDL function

CEC, HDL-induced nitric oxide and superoxide production in endothelial cells as well as serum PON-1 activity show good precision within specialized labs [95,96,97[■],98] but accuracy and agreement of measurements between labs are unknown because of lacking reference material and absence of systematic external quality assessment surveys. Efflux of radiolabeled cholesterol and efflux of a fluorescent cholesterol analogue from J774 cells showed rather poor agreement with a coefficient of correlation of 0.52 [97[■]]. Nevertheless, upon either method low CEC from J774 cells predicted cardiovascular events in three prospective cohort studies [97[■],99[■],100[■]]. By contrast, CEC as determined by the use of RAW cells or THP1 cells as the cholesterol donors did not show the inverse association with cardiovascular events during the follow-up of patients who underwent diagnostic coronary angiography and kidney transplantation, respectively [101,102[■]]. Rather by contrast, CEC determined in the presence of RAW cells was positively associated with the incidence of cardiovascular events, although it showed very good agreement with CEC determined from J774 cells ($r=0.92$) [101]. In the kidney-transplanted patients, CEC from THP1 cells was independently associated with graft survival but not with cardiovascular events or mortality [102[■]]. The increase in CEC but lack of clinical efficacy upon treatment with dalcetrapib or evacetrapib [103,104] indirectly question the utility of CEC to aid in drug development or monitoring of treatment success. Laborious and artifact-prone ultracentrifugation [105] limits the feasibility of bioassays such as recording of endothelial and anti-inflammatory functionalities in large sample numbers of clinical or epidemiological studies. Nevertheless, systematic head to head comparisons are needed to establish the HDL functionality which has the strongest association with CHD and treatment response and is, therefore, likely most relevant for the antiatherogenicity of HDLs.

HDL components

Apart from HDL-C, apoA-I has been most extensively investigated for its association with incident CHD. Overall apoA-I and HDL-C appear to have

similar prognostic values [3,4]. Meta-analyses of statin trials revealed that on-treatment changes of apoA-I levels but not on-treatment changes of HDL-C are associated with outcome. However, the association is too weak for clinical utility [4].

Structure-function relationships of HDLs' function and dysfunction are not comprehensively elaborated. Most of them have been detected by explorative parallel functional, proteomic, lipidomic, or transcriptomic characterization of HDLs in relatively small case-control studies [25[■],48–50,51[■],56,57]. Only a few of them have been validated in larger longitudinal studies. The significant inverse association between PON1 activity and CHD was shown in several studies. It appears to be stronger in diabetic patients than in nondiabetic subjects [29]. In the Physician's Health and Nurses Health Studies, cholesterol in apoC-III-containing HDLs showed a positive association with incident CHD, whereas cholesterol in apoC-III-free HDLs showed the expected inverse association [106]. In diabetic patients on hemodialysis, a high SAA content of HDLs was associated with increased risk of cardiovascular events and death [107]. Interestingly, in the same study, cohort levels of apoA-II but not apoA-I or HDL-C were predictors of cardiovascular morbidity and total mortality [108]. In the LURIC study of 3310 patients undergoing coronary angiography, plasma levels of SAA and HDL-C were found to interact: in patients with plasma SAA levels below the 80th percentile, HDL-C showed the expected inverse association with all-cause and cardiovascular mortality. In patients with elevated SAA levels, the opposite associations were found [51[■]]. Based on these findings, the authors derived a formula to calculate 'biologically effective HDL-C'. In two replication studies, one on the hemodialysis patients mentioned before and the other in the population-based cooperative health research in the region of Augsburg cohort, 'biologically effective HDL-C' but not measured HDL-C predicted outcome [51[■]].

CONCLUSION

By their many functions in innate host defense, HDLs remain interesting targets for the clinical management of diseases, even beyond CVD. However, any successful clinical exploitation will depend on the identification of the most relevant (dys)functions and their structural correlates. This needs a study that comprehensively characterizes HDLs of healthy and diseased donors for structure (particle size by NMR and particle composition by proteomics, lipidomics, miRNA transcriptomics) and function (diverse bioassays, e.g., on CEC from macrophages and eNOS activation in endothelial

cells). Combined with bioinformatics such a systems biological approach may prioritize (dys)functions and components which are most strongly correlated with each other and most closely associated with disease states. The most stringent structure-(dys)function-phenotype relationships will provide biomarker candidates to improve risk assessment and monitoring of treatment response. The most relevant agonists of either functional or dysfunctional HDLs are interesting targets for drug development, either directly themselves or indirectly by unravelling their downstream cellular responders as therapeutic targets. Mediators of physiological protective functions would need activation, whereas mediators of HDL dysfunction would need inhibition. Lost functional HDL components would need replenishment, for example, by HDL mimetics [109] or activation. Mediators of dominant negative dysfunctions must be either eliminated or inhibited in formation or action. Any therapy that prolongs the residence time of HDLs with gained dysfunction will be rather harmful, even if it increases HDL-C levels.

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Conflicts of interest

There are no conflicts of interest.

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Papers of particular interest, published within the annual period of review, have been highlighted as:

- of special interest
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